

# X-Ray Reconstruction of Moving Morphology (XROMM)

**CRITICAL UPDATE: Use new XMA Lab software for marker-based XROMM, and also for undistorting and calibrating biplanar X-ray setups.**

**XMA Lab replaces MATLAB XrayProject. See Bitbucket XMA Lab wiki for XMA Lab User Manual (not this wiki).**

**Note: there is a Table of Contents we recommend you use to navigate this xrommwiki. The links on this page are obsolete.**

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X-Ray Reconstruction of Moving Morphology (XROMM) is an X-ray imaging and computational process that produces precise and accurate 3D movies of skeletal movement.

*z\_\****OBSOLETE\*** *Recent Changes and DOWNLOADS*

*Brown XROMM Short Courses*

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**At Brown University we have developed three main approaches to XROMM:**

- 1) **Marker-based XROMM workflow (Brainerd et al., 2010)**
- 2) **Scientific Rotoscoping workflow, i.e. manual markerless XROMM (Gatesy et al., 2010)**
- 3) **XROMM AutoScoper software, i.e. automated markerless XROMM (Miranda et al., 2011)**

*New: XROMM Undistorter, stand-alone undistortion program*

We have also developed the X-ray Motion Analysis Portal (**XMA Portal**) for storing, viewing and managing X-ray movie data and associated metadata.

**Resources for Keck Foundation XROMM Core Facility**

**This wiki contains instructions and software downloads, contributed by many users. See [www.xromm.org](http://www.xromm.org) and the publications below for general information about XROMM.**

Brainerd, E.L., D.B. Baier, S.M. Gatesy, T.L. Hedrick, K.A. Metzger, S.L. Gilbert, and J.J. Crisco. (2010) X-ray Reconstruction of Moving Morphology (XROMM): precision, accuracy and applications in comparative biomechanics research. *Journal of Experimental Zoology*, 313A: 262-279.

Gatesy S.M., Baier D.B., Jenkins F.A., Dial K.P. (2010) Scientific rotoscoping: a morphology-based method of 3-D motion analysis and visualization. *Journal of Experimental Zoology*, 313A:244-261.

Miranda, D.L., Schwartz, J.B., Loomis, A.C., Brainerd, E.L., Fleming, B.C., Crisco, J.J. (2011) Static and Dynamic Error of a Biplanar Videoradiography System Using Marker-Based and Markerless Tracking Techniques. *Journal of Biomechanical Engineering*, 133 (12): 1-8.

Knorlein, B.J., Baier, D.B., Gatesy, S.M., Laurence-Chasen, J.D. and Brainerd, E.L. 2016. Validation of XMA Lab software for marker-based XROMM. *Journal of Experimental Biology*, 219: 3701-3711. doi: 10.1242/jeb.145383.

